

**RAW SEQUENCE LISTING  
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/635,521

Source: OIPE

Date Processed by STIC: 8/18/00

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.**

**FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,  
703-308-4212.**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW**

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/635,521</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies primarily to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: <b>(2) INFORMATION FOR SEQ ID NO:X:</b> <b>(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")</b> <b>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:</b> <b>This sequence is intentionally skipped</b>  Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence. <b>&lt;210&gt; sequence id number</b> <b>&lt;400&gt; sequence id number</b> <b>000</b>	
10 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing this mandatory field or its response.	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/635,521

DATE: 08/18/2000  
TIME: 14:12:07

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\08182000\I635521.raw

3 <110> APPLICANT: Katherine Galvin and Laura A. Rudolph-Owen  
 5 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND  
 6 DIAGNOSIS OF CARDIOVASCULAR DISEASE USING GPCR 4941 AS  
 7 A TARGET  
 9 <130> FILE REFERENCE: MNI-094  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/635,521  
 C--> 12 <141> CURRENT FILING DATE: 2000-08-09  
 14 <150> PRIOR APPLICATION NUMBER: 60/199,908  
 15 <151> PRIOR FILING DATE: 2000-04-26  
 17 <160> NUMBER OF SEQ ID NOS: 3  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 1362  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Homo sapiens  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS /  
 28 <222> LOCATION: (1)..(1359)  
 30 <400> SEQUENCE: 1  
 31 atg gct tca ccc agc ctc ccg ggc agt gac tgc tcc caa atc att gat 48  
 32 Met Ala Ser Pro Ser Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp  
 33 1 5 10 15  
 35 cac agt cat gtc ccc gag ttt gag gtg gcc acc tgg atc aaa atc acc 96  
 36 His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr  
 37 20 25 30  
 39 ctt att ctg gtg tac ctg atc atc ttc gtg atg ggc ctt ctg ggg aac 144  
 40 Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn  
 41 35 40 45  
 43 agc gcc acc att cgg gtc acc cag gtg ctg cag aag aaa gga tac ttg 192  
 44 Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu  
 45 50 55 60  
 47 cag aag gag gtg aca gac cac atg gtg agt ttg gct tgc tcg gac atc 240  
 48 Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile  
 49 65 70 75 80  
 51 ttg gtg ttc ctc atc ggc atg ccc atg gag ttc tac agc atc atc tgg 288  
 52 Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp  
 53 85 90 95  
 55 aat ccc ctg acc acg tcc agc tac acc ctg tcc tgc aag ctg cac act 336  
 56 Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr  
 57 100 105 110  
 59 ttc ctc ttc gag gcc tgc agc tac gct acg ctg ctg cac gtg ctg aca 384  
 60 Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr  
 61 115 120 125  
 63 ctc agc ttt gag cgc tac atc gcc atc tgt cac ccc ttc agg tac aag 432  
 64 Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys  
 65 130 135 140  
 67 gct gtg tcg gga cct tgc cag gtg aag ctg ctg att ggc ttc gtc tgg 480

Does Not Comply  
Corrected Diskette Needed

See P. 7

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/635,521

DATE: 08/18/2000  
TIME: 14:12:07

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\08182000\I635521.raw

68 Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp	
69 145 150 155 160	
71 gtc acc tcc gcc ctg gtg gca ctg ccc ttg ctg ttt gcc atg ggt act	528
72 Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr	
73 165 170 175	
75 gag tac ccc ctg gtg aac gtg ccc agc cac cgg ggt ctc act tgc aac	576
76 Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn	
77 180 185 190	
79 cgc tcc agc acc cgc cac cac gag cag ccc gag acc tcc aat atg tcc	624
80 Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser	
81 195 200 205	
83 atc tgt acc aac ctc tcc agc cgc tgg acc gtg ttc cag tcc agc atc	672
84 Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile	
85 210 215 220	
87 ttc ggc gcc ttc gtg gtc tac ctc gtg gtc ctc tcc gta gcc ttc	720
88 Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe	
89 225 230 235 240	
91 atg tgc tgg aac atg atg cag gtg ctc atg aaa agc cag aag ggc tcg	768
92 Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser	
93 245 250 255	
95 ctg gcc ggg ggc acg cgg cct ccg cag ctg agg aag tcc gag agc gaa	816
96 Leu Ala Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu	
97 260 265 270	
99 gag agc agg acc gcc agg agg cag acc atc atc ttc ctg agg ctg att	864
100 Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile	
101 275 280 285	
103 gtt gtg aca ttg gcc gta tgc tgg atg ccc aac cag att cgg agg atc	912
104 Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile	
105 290 295 300	
107 atg gct gcg gcc aaa ccc aag cac gac tgg acg agg tcc tac ttc cgg	960
108 Met Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg	
109 305 310 315 320	
111 gcg tac atg atc ctc ctc ccc ttc tcg gag acg ttt ttc tac ctc agc	1008
112 Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser	
113 325 330 335	
115 tcg gtc atc aac ccg ctc ctg tac acg gtg tcc tcg cag cag ttt cgg	1056
116 Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg	
117 340 345 350	
119 cgg gtg ttc gtg cag gtg ctg tgc cgc ctg tcg ctg cag cac gcc	1104
120 Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala	
121 355 360 365	
123 aac cac gag aag cgc ctg cgc gta cat gcg cac tcc acc acc gac agc	1152
124 Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser	
125 370 375 380	
127 gcc cgc ttt gtg cag cgc ccg ttg ctc ttc gcg tcc cgg cgc cag tcc	1200
128 Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser	
129 385 390 395 400	
131 tct gca agg aga act gag aag att ttc tta agc act ttt cag agc gag	1248
132 Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu	

RAW SEQUENCE LISTING DATE: 08/18/2000  
 PATENT APPLICATION: US/09/635,521 TIME: 14:12:07

Input Set : A:\seqlist.txt  
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133	405	410	415	
135	gcc gag ccc cag tct aag tcc cag tca ttg agt ctc gag tca cta gag			1296
136	Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu			
137	420	425	430	
139	ccc aac tca ggc gcg aaa cca gcc aat tct gct gca gag aat ggt ttt			1344
140	Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe			
141	435	440	445	
143	cag gag cat gaa gtt' tga			1362
144	Gln Glu His Glu Val			
145	450			
148	<210> SEQ ID NO: 2			
149	<211> LENGTH: 453			
150	<212> TYPE: PRT			
151	<213> ORGANISM: Homo sapiens			
153	<400> SEQUENCE: 2			
154	Met Ala Ser Pro Ser Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp			
155	1	5	10	15
157	His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr			
158	20	25	30	
160	Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn			
161	35	40	45	
163	Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu			
164	50	55	60	
166	Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile			
167	65	70	75	80
169	Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp			
170	85	90	95	
172	Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr			
173	100	105	110	
175	Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr			
176	115	120	125	
178	Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys			
179	130	135	140	
181	Ala Val Ser Gly Pro Cys Gln Val Lys Leu Ile Gly Phe Val Trp			
182	145	150	155	160
184	Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr			
185	165	170	175	
187	Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn			
188	180	185	190	
190	Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser			
191	195	200	205	
193	Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile			
194	210	215	220	
196	Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe			
197	225	230	235	240
199	Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser			
200	245	250	255	
202	Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu			
203	260	265	270	

**VERIFICATION SUMMARY** DATE: 08/18/2000  
**PATENT APPLICATION:** US/09/635,521 **TIME:** 14:12:08

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\08182000\I635521.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:404 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
L:404 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3